



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/900,380
Source: FWS
Date Processed by STIC: 11/19/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORRED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <i>10/700,380</i>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
TIME: 16:41:40

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

3 <110> APPLICANT: Timmermans, Eveline
4 C.A.C.
7 van Gemen, Bob
W--> 8 <120> TITLE OF INVENTION: Method for Quantifying a Ratio Between at Least
W--> 9 Two Nucleic Acid Sequences
W--> 10 <130> FILE REFERENCE: 2183-5581.1US
W--> 11 <140> CURRENT APPLICATION NUMBER: To be Assigned
14 <141> CURRENT FILING DATE: 2003-11-03
15 <150> PRIOR APPLICATION NUMBER: 60/425,055
16 <151> PRIOR FILING DATE: 2002-11-08
W--> 17 <160> NUMBER OF SEQ ID: 18
18 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

W--> 19 <210> SEQ ID NO: 1
20 <211> LENGTH: 48
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial sequence
W--> 23 <220> FEATURE:
24 <223> OTHER INFORMATION: Synthesized sequence, primer MtD p1
W--> 26 <400> SEQUENCE: 1
E--> 27 aattctaata cgactcaacta tagggagaag
28 agccgtttag ttgtggta 48
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 25
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial sequence
W--> 33 <220> FEATURE:
34 <223> OTHER INFORMATION: Synthesized sequence, primer MtD p2
W--> 36 <400> SEQUENCE: 2
E--> 37 tctccatcta ttgatgaggg tctta
38 25
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 49
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial sequence
W--> 43 <220> FEATURE:
44 <223> OTHER INFORMATION: Synthesized sequence, MtD p1_2
W--> 45 <400> SEQUENCE: 3

ppn 1-5
IMPORTANT: Please
ensure that file is saved
in ASCII text
format (per
rule 1.824)
Sequence
(global error) Rules)
see item 1 on Error Summary
Sheet
same errors

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Input Set : A:\PTO.YF.txt
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E--> 46 aattctaata cgactcacta taggaaagaa → same
 47 cggggctctg ccatcttaa 49
 48 <210> SEQ ID NO: 4
 49 <211> LENGTH: 20
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial sequence
 W--> 52 <220> FEATURE:
 53 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 54 p2_2 → same
 56 <400> SEQUENCE: 4
 E--> 57 gtaatccagg tcgggttctta
 58 20 →
 59 <210> SEQ ID NO: 5
 60 <211> LENGTH: 32
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Artificial sequence
 W--> 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 65 mb_2 →
 W--> 66 <400> SEQUENCE: 5
 E--> 67 gaccccccacccaccca agaacagggt cc → same
 68 32 →
 69 <210> SEQ ID NO: 6
 70 <211> LENGTH: 49
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Artificial sequence
 W--> 73 <220> FEATURE:
 74 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
 75 p1 →
 W--> 76 <400> SEQUENCE: 6
 E--> 77 aattctaata cgactcacta tagggagagg →
 78 cccggcatgt ggtgcataa 49
 79 <210> SEQ ID NO: 7
 80 <211> LENGTH: 23
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Artificial sequence
 W--> 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
 85 p2 →
 W--> 86 <400> SEQUENCE: 7
 E--> 87 ttccttacat ctctcacccg cta
 88 23 →
 89 <210> SEQ ID NO: 8
 90 <211> LENGTH: 20
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial sequence
 W--> 93 <220> FEATURE:
 94 <223> OTHER INFORMATION: Synthesized sequence, primer
 95 SnrpD2 p2 →

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Input Set : A:\PTO.YF.txt
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W--> 96 <400> SEQUENCE: 8
E--> 97 tgccgcattt tctgggtgtt *same*
98 20
99 <210> SEQ ID NO: 9
100 <211> LENGTH: 34
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial sequence
W--> 103 <220> FEATURE:
104 <223> OTHER INFORMATION: Synthesized sequence, primer
105 SnrnpD mb_2
W--> 106 <400> SEQUENCE: 9
E--> 107 cgcgtgtgtt aaccacgcac ttcctcgca tgcc *same*
108 34
109 <210> SEQ ID NO: 10
110 <211> LENGTH: 34
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial sequence
W--> 113 <220> FEATURE:
114 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
115 mb
W--> 116 <400> SEQUENCE: 10
E--> 117 gctccgaagc ttctgactct tacctcccg gagg *same*
118 34
119 <210> SEQ ID NO: 11
120 <211> LENGTH: 49
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial sequence
W--> 123 <220> FEATURE:
124 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
125 p1_4
W--> 126 <400> SEQUENCE: 11
E--> 127 aattctaata cgactcaacta tagggagagg *same*
128 agacacctgc taggtgtaa 49
129 <210> SEQ ID NO: 12
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial sequence
W--> 133 <220> FEATURE:
134 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
135 p2_2
W--> 136 <400> SEQUENCE: 12
E--> 137 ggtccccccg atatggcgtt cc *same*
138 22
139 <210> SEQ ID NO: 13
140 <211> LENGTH: 49
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial sequence
W--> 143 <220> FEATURE:
144 <223> OTHER INFORMATION: Synthesized sequence, primer Sig

RAW SEQUENCE LISTING
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Input Set : A:\PTO.YF.txt
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145 p1
W--> 146 <400> SEQUENCE: 13
E--> 147 aattctaata cgactcacta tagggagagg *same*
 148 actggccct cagcctgca 49
 149 <210> SEQ ID NO: 14
 150 <211> LENGTH: 21
 151 <212> TYPE: DNA
 152 <213> ORGANISM: Artificial sequence
W--> 153 <220> FEATURE:
 154 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
 155 p2
W--> 156 <400> SEQUENCE: 14
E--> 157 ctgaggagac aaggaccatc a *same*
 158 21
 159 <210> SEQ ID NO: 15
 160 <211> LENGTH: 32
 161 <212> TYPE: DNA
 162 <213> ORGANISM: Artificial sequence
W--> 163 <220> FEATURE:
 164 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
 165 mb
W--> 166 <400> SEQUENCE: 15
E--> 167 cgtacgaatg acgtccccct gcgaatcgta cg *same*
 168 32
 169 <210> SEQ ID NO: 16
 170 <211> LENGTH: 49
 171 <212> TYPE: DNA
 172 <213> ORGANISM: Artificial sequence
W--> 173 <220> FEATURE:
 174 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
 175 p1
W--> 176 <400> SEQUENCE: 16
E--> 177 aattctaata cgactcacta taggaaagag *same*
 178 ctctctcccttggccct 49
 179 <210> SEQ ID NO: 17
 180 <211> LENGTH: 24
 181 <212> TYPE: DNA
 182 <213> ORGANISM: Artificial sequence
W--> 183 <220> FEATURE:
 184 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
 185 p2
W--> 186 <400> SEQUENCE: 17
E--> 187 gcatctctgt tcatgactgt gtga *same*
 188 24
 189 <210> SEQ ID NO: 18
 190 <211> LENGTH: 33
 191 <212> TYPE: DNA
 192 <213> ORGANISM: Artificial sequence
W--> 193 <220> FEATURE:

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194 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
195 mb
W--> 196 <400> SEQUENCE: 18
E--> 197 cgtacgctca acgcccagcac gcgcgtaccgt acg
198 33 *Mane*

VERIFICATION SUMMARY

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TIME: 16:41:41

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

L:8 M:283 W: Missing Blank Line separator, <120> field identifier
L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:283 W: Missing Blank Line separator, <210> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:1
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:2
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:3
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:63 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:5
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:76 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:6
L:83 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:7
L:93 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:103 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:9
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:10
L:123 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:127 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:11
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:12
L:143 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:13
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:14
L:163 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY
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Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

L:166 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:15
L:173 M:283 W: Missing Blank Line separator, <220> field identifier
L:176 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:16
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:17
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:197 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18